

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Lovenberg, Timothy W.
Oltersdorf, Tilman
Liaw, Chen Wang
Grigoriadis, Dimitri E.
Chalmers, Derek T.
DeSouza, Errol B.
- (ii) TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR 2
RECEPTORS
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
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 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: USA
 - (F) ZIP: 98104-7092
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE: 09-APR-2004
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Christiansen, William T.
 - (B) REGISTRATION NUMBER: 44,614
 - (C) REFERENCE/DOCKET NUMBER: 690068.401C5
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1514 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 44..1336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GATCCCTATC CCTGAGCAAG CGAGTGGCAG GATCTGGTGT CCC	ATG GGG CAC CCA	55
	Met Gly His Pro	
	1	
GGC TCT CTT CCC AGT GCA CAA CTC CTC CTC TGC CTA TAC TCT CTG CTC		103
Gly Ser Leu Pro Ser Ala Gln Leu Leu Leu Cys Leu Tyr Ser Leu Leu		
5 10 15 20		
CCA CTG CTC CAG GTG GCC CAA CCA GGC AGG CCA CTC CAG GAC CAG CCC		151
Pro Leu Leu Gln Val Ala Gln Pro Gly Arg Pro Leu Gln Asp Gln Pro		
25 30 35		
CTG TGG ACA CTT TTG GAG CAG TAC TGC CAT AGG ACC ACA ACT CGG AAT		199
Leu Trp Thr Leu Leu Glu Gln Tyr Cys His Arg Thr Thr Thr Arg Asn		
40 45 50		
TTT TCA GGT CCC TAC TCC TAC TGC AAC ACG ACC TTG GAC CAG ATC GGG		247
Phe Ser Gly Pro Tyr Ser Tyr Cys Asn Thr Thr Leu Asp Gln Ile Gly		
55 60 65		
ACC TGC TGG CCC CAG AGC GCG CCT GGA GCC CTA GTG GAG AGA CCA TGC		295
Thr Cys Trp Pro Gln Ser Ala Pro Gly Ala Leu Val Glu Arg Pro Cys		
70 75 80		
CCC GAA TAC TTC AAC GGC ATC AAG TAC AAC ACG ACC CGG AAT GCC TAC		343
Pro Glu Tyr Phe Asn Gly Ile Lys Tyr Asn Thr Arg Asn Ala Tyr		
85 90 95 100		
AGA GAA TGC CTG GAG AAT GGG ACC TGG GCC TCA AGG ATC AAC TAC TCA		391
Arg Glu Cys Leu Glu Asn Gly Thr Trp Ala Ser Arg Ile Asn Tyr Ser		
105 110 115		
CAC TGT GAA CCC ATT TTG GAT GAC AAG CAG AGG AAG TAT GAC CTG CAT		439
His Cys Glu Pro Ile Leu Asp Asp Lys Gln Arg Lys Tyr Asp Leu His		
120 125 130		
TAC CGA ATC GCC CTC ATC ATC AAC TAC CTG GGC CAC TGT GTT TCC GTG		487
Tyr Arg Ile Ala Leu Ile Ile Asn Tyr Leu Gly His Cys Val Ser Val		
135 140 145		
GTG GCC CTG GTG GCT GCT TTC CTG CTT TTC CTA GTG CTG CGG AGT ATC		535
Val Ala Leu Val Ala Ala Phe Leu Leu Phe Leu Val Leu Arg Ser Ile		
150 155 160		
CGC TGC CTG CGG AAT GTG ATC CAC TGG AAC CTC ATC ACC ACC TTC ATC		583
Arg Cys Leu Arg Asn Val Ile His Trp Asn Leu Ile Thr Thr Phe Ile		
165 170 175 180		
CTG AGA AAC ATC ACG TGG TTC CTG CTG CAA CTC ATC GAC CAC GAA GTG		631
Leu Arg Asn Ile Thr Trp Phe Leu Leu Gln Leu Ile Asp His Glu Val		
185 190 195		
CAT GAG GGC AAT GAG GTC TGG TGC CGC TGC GTC ACC ACC ATA TTC AAC		679

His	Glu	Gly	Asn	Glu	Val	Trp	Cys	Arg	Cys	Val	Thr	Thr	Ile	Phe	Asn	
			200					205					210			
TAC	TTT	GTG	GTC	ACC	AAC	TTC	TTC	TGG	ATG	TTT	GTG	GAA	GGC	TGC	TAC	727
Tyr	Phe	Val	Val	Thr	Asn	Phe	Phe	Trp	Met	Phe	Val	Glu	Gly	Cys	Tyr	
		215					220					225				
CTG	CAC	ACG	GCC	ATC	GTC	ATG	ACG	TAC	TCC	ACG	GAG	CAT	CTG	CGC	AAG	775
Leu	His	Thr	Ala	Ile	Val	Met	Thr	Tyr	Ser	Thr	Glu	His	Leu	Arg	Lys	
		230				235					240					
TGG	CTC	TTC	CTC	TTC	ATT	GGA	TGG	TGC	ATA	CCC	TGC	CCT	ATC	ATT	GTC	823
Trp	Leu	Phe	Leu	Phe	Ile	Gly	Trp	Cys	Ile	Pro	Cys	Pro	Ile	Ile	Val	
245					250					255					260	
GCC	TGG	GCA	GTT	GGC	AAA	CTC	TAC	TAT	GAG	AAT	GAG	CAG	TGC	TGG	TTT	871
Ala	Trp	Ala	Val	Gly	Lys	Leu	Tyr	Tyr	Glu	Asn	Glu	Gln	Cys	Trp	Phe	
				265					270					275		
GGC	AAG	GAA	CCT	GGT	GAC	TTA	GTG	GAC	TAC	ATC	TAC	CAG	GGC	CCC	ATC	919
Gly	Lys	Glu	Pro	Gly	Asp	Leu	Val	Asp	Tyr	Ile	Tyr	Gln	Gly	Pro	Ile	
			280					285					290			
ATC	CTC	GTG	CTC	CTC	ATC	AAT	TTT	GTG	TTT	CTG	TTC	AAC	ATC	GTC	AGG	967
Ile	Leu	Val	Leu	Leu	Ile	Asn	Phe	Val	Phe	Leu	Phe	Asn	Ile	Val	Arg	
		295					300					305				
ATC	CTG	ATG	ACA	AAA	CTG	CGA	GCC	TCC	ACC	ACA	TCC	GAG	ACC	ATC	CAG	1015
Ile	Leu	Met	Thr	Lys	Leu	Arg	Ala	Ser	Thr	Thr	Ser	Glu	Thr	Ile	Gln	
		310				315					320					
TAC	AGG	AAG	GCA	GTG	AAG	GCC	ACC	CTG	GTC	CTC	CTC	CCC	CTG	TTG	GGC	1063
Tyr	Arg	Lys	Ala	Val	Lys	Ala	Thr	Leu	Val	Leu	Leu	Pro	Leu	Leu	Gly	
325					330					335					340	
ATC	ACC	TAC	ATG	CTC	TTC	TTT	GTC	AAT	CCT	GGA	GAG	GAC	GAC	CTG	TCA	1111
Ile	Thr	Tyr	Met	Leu	Phe	Phe	Val	Asn	Pro	Gly	Glu	Asp	Asp	Leu	Ser	
				345					350					355		
CAG	ATT	GTG	TTC	ATC	TAC	TTC	AAC	TCT	TTC	CTG	CAG	TCC	TTT	CAG	GGT	1159
Gln	Ile	Val	Phe	Ile	Tyr	Phe	Asn	Ser	Phe	Leu	Gln	Ser	Phe	Gln	Gly	
			360					365					370			
TTC	TTT	GTG	TCC	GTT	TTC	TAC	TGC	TTC	TTC	AAT	GGA	GAG	GTG	CGC	TCC	1207
Phe	Phe	Val	Ser	Val	Phe	Tyr	Cys	Phe	Phe	Asn	Gly	Glu	Val	Arg	Ser	
		375					380					385				
GCC	CTG	AGA	AAG	CGG	TGG	CAC	CGT	TGG	CAG	GAC	CAC	CAC	GCC	CTC	CGA	1255
Ala	Leu	Arg	Lys	Arg	Trp	His	Arg	Trp	Gln	Asp	His	His	Ala	Leu	Arg	
		390				395					400					
GTG	CCT	GTG	GCC	CGG	GCC	ATG	TCC	ATT	CCC	ACA	TCG	CCC	ACC	AGG	ATC	1303
Val	Pro	Val	Ala	Arg	Ala	Met	Ser	Ile	Pro	Thr	Ser	Pro	Thr	Arg	Ile	
405					410					415					420	
AGC	TTC	CAC	AGC	ATC	AAG	CAG	ACA	GCT	GCC	GTG	TGATCCCCTG	TCACCCATCT				1356
Ser	Phe	His	Ser	Ile	Lys	Gln	Thr	Ala	Ala	Val						

425	430	
CCCCAGCACT CCACCACCGA GCGGGCTTCC TCATTCTTCA CAGCCTTCCC TGGGTCCTCC		1416
TTGCTACACT GACCCTTGGG TGCAGGAGAA GGGGGGGTGG ATGAACTCTC CTGCCGGAAG		1476
AAAGGAAAAC TATGAAATGG AGGCTCTGAA AGACCAGG		1514

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	His	Pro	Gly	Ser	Leu	Pro	Ser	Ala	Gln	Leu	Leu	Leu	Cys	Leu	
1				5					10					15		
Tyr	Ser	Leu	Leu	Pro	Leu	Leu	Gln	Val	Ala	Gln	Pro	Gly	Arg	Pro	Leu	
			20					25					30			
Gln	Asp	Gln	Pro	Leu	Trp	Thr	Leu	Leu	Glu	Gln	Tyr	Cys	His	Arg	Thr	
			35				40					45				
Thr	Thr	Arg	Asn	Phe	Ser	Gly	Pro	Tyr	Ser	Tyr	Cys	Asn	Thr	Thr	Leu	
			50			55					60					
Asp	Gln	Ile	Gly	Thr	Cys	Trp	Pro	Gln	Ser	Ala	Pro	Gly	Ala	Leu	Val	
65					70					75					80	
Glu	Arg	Pro	Cys	Pro	Glu	Tyr	Phe	Asn	Gly	Ile	Lys	Tyr	Asn	Thr	Thr	
				85					90					95		
Arg	Asn	Ala	Tyr	Arg	Glu	Cys	Leu	Glu	Asn	Gly	Thr	Trp	Ala	Ser	Arg	
			100					105					110			
Ile	Asn	Tyr	Ser	His	Cys	Glu	Pro	Ile	Leu	Asp	Asp	Lys	Gln	Arg	Lys	
			115				120					125				
Tyr	Asp	Leu	His	Tyr	Arg	Ile	Ala	Leu	Ile	Ile	Asn	Tyr	Leu	Gly	His	
			130			135					140					
Cys	Val	Ser	Val	Val	Ala	Leu	Val	Ala	Ala	Phe	Leu	Leu	Phe	Leu	Val	
145					150					155					160	
Leu	Arg	Ser	Ile	Arg	Cys	Leu	Arg	Asn	Val	Ile	His	Trp	Asn	Leu	Ile	
				165					170					175		
Thr	Thr	Phe	Ile	Leu	Arg	Asn	Ile	Thr	Trp	Phe	Leu	Leu	Gln	Leu	Ile	
			180				185						190			
Asp	His	Glu	Val	His	Glu	Gly	Asn	Glu	Val	Trp	Cys	Arg	Cys	Val	Thr	

195					200					205					
Thr	Ile	Phe	Asn	Tyr	Phe	Val	Val	Thr	Asn	Phe	Phe	Trp	Met	Phe	Val
	210					215					220				
Glu	Gly	Cys	Tyr	Leu	His	Thr	Ala	Ile	Val	Met	Thr	Tyr	Ser	Thr	Glu
225					230					235					240
His	Leu	Arg	Lys	Trp	Leu	Phe	Leu	Phe	Ile	Gly	Trp	Cys	Ile	Pro	Cys
				245					250					255	
Pro	Ile	Ile	Val	Ala	Trp	Ala	Val	Gly	Lys	Leu	Tyr	Tyr	Glu	Asn	Glu
			260					265					270		
Gln	Cys	Trp	Phe	Gly	Lys	Glu	Pro	Gly	Asp	Leu	Val	Asp	Tyr	Ile	Tyr
		275					280					285			
Gln	Gly	Pro	Ile	Ile	Leu	Val	Leu	Leu	Ile	Asn	Phe	Val	Phe	Leu	Phe
	290					295					300				
Asn	Ile	Val	Arg	Ile	Leu	Met	Thr	Lys	Leu	Arg	Ala	Ser	Thr	Thr	Ser
305					310					315					320
Glu	Thr	Ile	Gln	Tyr	Arg	Lys	Ala	Val	Lys	Ala	Thr	Leu	Val	Leu	Leu
				325					330					335	
Pro	Leu	Leu	Gly	Ile	Thr	Tyr	Met	Leu	Phe	Phe	Val	Asn	Pro	Gly	Glu
			340					345					350		
Asp	Asp	Leu	Ser	Gln	Ile	Val	Phe	Ile	Tyr	Phe	Asn	Ser	Phe	Leu	Gln
		355					360					365			
Ser	Phe	Gln	Gly	Phe	Phe	Val	Ser	Val	Phe	Tyr	Cys	Phe	Phe	Asn	Gly
	370					375					380				
Glu	Val	Arg	Ser	Ala	Leu	Arg	Lys	Arg	Trp	His	Arg	Trp	Gln	Asp	His
385					390					395					400
His	Ala	Leu	Arg	Val	Pro	Val	Ala	Arg	Ala	Met	Ser	Ile	Pro	Thr	Ser
				405					410					415	
Pro	Thr	Arg	Ile	Ser	Phe	His	Ser	Ile	Lys	Gln	Thr	Ala	Ala	Val	
			420					425					430		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1626 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 216..1449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCGGCCCCCTC ATCTCCGTGA GCGCCGAGGC TTCTCTTGGC CAAGGTCCTA GGAGTGATCC	60
GATTGAGAGC GGCGCCCCAA AGCTGCCGGG CTGGCCGGGG TGGGCGGGGA GGCACCTGGA	120
CGCTGCACTC TCTGGTGGCT CCGCGTCGCG CCAGGTCCCT CGCAGCCACG CGGGGCGCGC	180
ACTCCCACTC CCAACGCGCG CGGCTCCGGA GCGCA ATG GAC GCG GCG CTG CTC	233
Met Asp Ala Ala Leu Leu	
1 5	
CTC AGC CTG CTG GAG GCC AAC TGC AGC CTG GCA CTG GCC GAA GAG CTG	281
Leu Ser Leu Leu Glu Ala Asn Cys Ser Leu Ala Leu Ala Glu Glu Leu	
10 15 20	
CTT TTG GAC GGC TGG GGA GAG CCC CCG GAC CCC GAA GGT CCC TAC TCC	329
Leu Leu Asp Gly Trp Gly Glu Pro Pro Asp Pro Glu Gly Pro Tyr Ser	
25 30 35	
TAC TGC AAC ACG ACC TTG GAC CAG ATC GGG ACC TGC TGG CCC CAG AGC	377
Tyr Cys Asn Thr Thr Leu Asp Gln Ile Gly Thr Cys Trp Pro Gln Ser	
40 45 50	
GCG CCT GGA GCC CTA GTG GAG AGA CCA TGC CCC GAA TAC TTC AAC GGC	425
Ala Pro Gly Ala Leu Val Glu Arg Pro Cys Pro Glu Tyr Phe Asn Gly	
55 60 65 70	
ATC AAG TAC AAC ACG ACC CGG AAT GCC TAC AGA GAA TGC CTG GAG AAT	473
Ile Lys Tyr Asn Thr Thr Arg Asn Ala Tyr Arg Glu Cys Leu Glu Asn	
75 80 85	
GGG ACC TGG GCC TCA AGG ATC AAC TAC TCA CAC TGT GAA CCC ATT TTG	521
Gly Thr Trp Ala Ser Arg Ile Asn Tyr Ser His Cys Glu Pro Ile Leu	
90 95 100	
GAT GAC AAG CAG AGG AAG TAT GAC CTG CAT TAC CGA ATC GCC CTC ATC	569
Asp Asp Lys Gln Arg Lys Tyr Asp Leu His Tyr Arg Ile Ala Leu Ile	
105 110 115	
ATC AAC TAC CTG GGC CAC TGT GTT TCC GTG GTG GCC CTG GTG GCT GCT	617
Ile Asn Tyr Leu Gly His Cys Val Ser Val Val Ala Leu Val Ala Ala	
120 125 130	
TTC CTG CTT TTC CTA GTG CTG CGG AGT ATC CGC TGC CTG CGG AAT GTG	665
Phe Leu Leu Phe Leu Val Leu Arg Ser Ile Arg Cys Leu Arg Asn Val	
135 140 145 150	
ATC CAC TGG AAC CTC ATC ACC ACC TTC ATC CTG AGA AAC ATC ACG TGG	713
Ile His Trp Asn Leu Ile Thr Thr Phe Ile Leu Arg Asn Ile Thr Trp	
155 160 165	
TTC CTG CTG CAA CTC ATC GAC CAC GAA GTG CAT GAG GGC AAT GAG GTC	761
Phe Leu Leu Gln Leu Ile Asp His Glu Val His Glu Gly Asn Glu Val	
170 175 180	

TGG	TGC	CGC	TGC	GTC	ACC	ACC	ATA	TTC	AAC	TAC	TTT	GTG	GTC	ACC	AAC	809
Trp	Cys	Arg	Cys	Val	Thr	Thr	Ile	Phe	Asn	Tyr	Phe	Val	Val	Thr	Asn	
		185					190					195				
TTC	TTC	TGG	ATG	TTT	GTG	GAA	GGC	TGC	TAC	CTG	CAC	ACG	GCC	ATC	GTC	857
Phe	Phe	Trp	Met	Phe	Val	Glu	Gly	Cys	Tyr	Leu	His	Thr	Ala	Ile	Val	
	200					205					210					
ATG	ACG	TAC	TCC	ACG	GAG	CAT	CTG	CGC	AAG	TGG	CTC	TTC	CTC	TTC	ATT	905
Met	Thr	Tyr	Ser	Thr	Glu	His	Leu	Arg	Lys	Trp	Leu	Phe	Leu	Phe	Ile	
215					220					225					230	
GGA	TGG	TGC	ATA	CCC	TGC	CCT	ATC	ATT	GTC	GCC	TGG	GCA	GTT	GGC	AAA	953
Gly	Trp	Cys	Ile	Pro	Cys	Pro	Ile	Ile	Val	Ala	Trp	Ala	Val	Gly	Lys	
				235					240					245		
CTC	TAC	TAT	GAG	AAT	GAG	CAG	TGC	TGG	TTT	GGC	AAG	GAA	CCT	GGT	GAC	1001
Leu	Tyr	Tyr	Glu	Asn	Glu	Gln	Cys	Trp	Phe	Gly	Lys	Glu	Pro	Gly	Asp	
			250					255					260			
TTA	GTG	GAC	TAC	ATC	TAC	CAG	GGC	CCC	ATC	ATC	CTC	GTG	CTC	CTC	ATC	1049
Leu	Val	Asp	Tyr	Ile	Tyr	Gln	Gly	Pro	Ile	Ile	Leu	Val	Leu	Leu	Ile	
		265					270					275				
AAT	TTT	GTG	TTT	CTG	TTC	AAC	ATC	GTC	AGG	ATC	CTG	ATG	ACA	AAA	CTG	1097
Asn	Phe	Val	Phe	Leu	Phe	Asn	Ile	Val	Arg	Ile	Leu	Met	Thr	Lys	Leu	
	280					285					290					
CGA	GCC	TCC	ACC	ACA	TCC	GAG	ACC	ATC	CAG	TAC	AGG	AAG	GCA	GTG	AAG	1145
Arg	Ala	Ser	Thr	Thr	Ser	Glu	Thr	Ile	Gln	Tyr	Arg	Lys	Ala	Val	Lys	
295					300					305					310	
GCC	ACC	CTG	GTC	CTC	CTC	CCC	CTG	TTG	GGC	ATC	ACC	TAC	ATG	CTC	TTC	1193
Ala	Thr	Leu	Val	Leu	Leu	Pro	Leu	Leu	Gly	Ile	Thr	Tyr	Met	Leu	Phe	
				315					320					325		
TTT	GTC	AAT	CCT	GGA	GAG	GAC	GAC	CTG	TCA	CAG	ATT	GTG	TTC	ATC	TAC	1241
Phe	Val	Asn	Pro	Gly	Glu	Asp	Asp	Leu	Ser	Gln	Ile	Val	Phe	Ile	Tyr	
			330					335					340			
TTC	AAC	TCT	TTC	CTG	CAG	TCC	TTT	CAG	GGT	TTC	TTT	GTG	TCC	GTT	TTC	1289
Phe	Asn	Ser	Phe	Leu	Gln	Ser	Phe	Gln	Gly	Phe	Phe	Val	Ser	Val	Phe	
		345					350					355				
TAC	TGC	TTC	TTC	AAT	GGA	GAG	GTG	CGC	TCC	GCC	CTG	AGA	AAG	CGG	TGG	1337
Tyr	Cys	Phe	Phe	Asn	Gly	Glu	Val	Arg	Ser	Ala	Leu	Arg	Lys	Arg	Trp	
	360					365					370					
CAC	CGT	TGG	CAG	GAC	CAC	CAC	GCC	CTC	CGA	GTG	CCT	GTG	GCC	CGG	GCC	1385
His	Arg	Trp	Gln	Asp	His	His	Ala	Leu	Arg	Val	Pro	Val	Ala	Arg	Ala	
375					380					385					390	
ATG	TCC	ATT	CCC	ACA	TCG	CCC	ACC	AGG	ATC	AGC	TTC	CAC	AGC	ATC	AAG	1433
Met	Ser	Ile	Pro	Thr	Ser	Pro	Thr	Arg	Ile	Ser	Phe	His	Ser	Ile	Lys	
				395					400						405	

CAG ACA GCT GCC GTG T GATCCCCTGT CACCCATCTG CCCAGCACTC 1479
 Gln Thr Ala Ala Val
 410

CACCACCGAG GCGGCTTCCT CATTCTTCAC AGCCTTCCCT GGGTCCTCCT TGCTACACTG 1539

ACCCTTGGGT GCAGGAGAAG GGGGGGTGGA TGAACCTCTCC TGCCGGAAGA AAGGAAAAC 1599

ATGAAATGGA GGCTCTGAAA GACCAGG 1626

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asp	Ala	Ala	Leu	Leu	Leu	Ser	Leu	Leu	Glu	Ala	Asn	Cys	Ser	Leu	1	5	10	15
Ala	Leu	Ala	Glu	Glu	Leu	Leu	Leu	Asp	Gly	Trp	Gly	Glu	Pro	Pro	Asp	20	25	30	
Pro	Glu	Gly	Pro	Tyr	Ser	Tyr	Cys	Asn	Thr	Thr	Leu	Asp	Gln	Ile	Gly	35	40	45	
Thr	Cys	Trp	Pro	Gln	Ser	Ala	Pro	Gly	Ala	Leu	Val	Glu	Arg	Pro	Cys	50	55	60	
Pro	Glu	Tyr	Phe	Asn	Gly	Ile	Lys	Tyr	Asn	Thr	Thr	Arg	Asn	Ala	Tyr	65	70	75	80
Arg	Glu	Cys	Leu	Glu	Asn	Gly	Thr	Trp	Ala	Ser	Arg	Ile	Asn	Tyr	Ser	85	90	95	
His	Cys	Glu	Pro	Ile	Leu	Asp	Asp	Lys	Gln	Arg	Lys	Tyr	Asp	Leu	His	100	105	110	
Tyr	Arg	Ile	Ala	Leu	Ile	Ile	Asn	Tyr	Leu	Gly	His	Cys	Val	Ser	Val	115	120	125	
Val	Ala	Leu	Val	Ala	Ala	Phe	Leu	Leu	Phe	Leu	Val	Leu	Arg	Ser	Ile	130	135	140	
Arg	Cys	Leu	Arg	Asn	Val	Ile	His	Trp	Asn	Leu	Ile	Thr	Thr	Phe	Ile	145	150	155	160
Leu	Arg	Asn	Ile	Thr	Trp	Phe	Leu	Leu	Gln	Leu	Ile	Asp	His	Glu	Val	165	170	175	
His	Glu	Gly	Asn	Glu	Val	Trp	Cys	Arg	Cys	Val	Thr	Thr	Ile	Phe	Asn	180	185	190	

Tyr Phe Val Val Thr Asn Phe Phe Trp Met Phe Val Glu Gly Cys Tyr
 195 200 205
 Leu His Thr Ala Ile Val Met Thr Tyr Ser Thr Glu His Leu Arg Lys
 210 215 220
 Trp Leu Phe Leu Phe Ile Gly Trp Cys Ile Pro Cys Pro Ile Ile Val
 225 230 235 240
 Ala Trp Ala Val Gly Lys Leu Tyr Tyr Glu Asn Glu Gln Cys Trp Phe
 245 250 255
 Gly Lys Glu Pro Gly Asp Leu Val Asp Tyr Ile Tyr Gln Gly Pro Ile
 260 265 270
 Ile Leu Val Leu Leu Ile Asn Phe Val Phe Leu Phe Asn Ile Val Arg
 275 280 285
 Ile Leu Met Thr Lys Leu Arg Ala Ser Thr Thr Ser Glu Thr Ile Gln
 290 295 300
 Tyr Arg Lys Ala Val Lys Ala Thr Leu Val Leu Leu Pro Leu Leu Gly
 305 310 315 320
 Ile Thr Tyr Met Leu Phe Phe Val Asn Pro Gly Glu Asp Asp Leu Ser
 325 330 335
 Gln Ile Val Phe Ile Tyr Phe Asn Ser Phe Leu Gln Ser Phe Gln Gly
 340 345 350
 Phe Phe Val Ser Val Phe Tyr Cys Phe Phe Asn Gly Glu Val Arg Ser
 355 360 365
 Ala Leu Arg Lys Arg Trp His Arg Trp Gln Asp His His Ala Leu Arg
 370 375 380
 Val Pro Val Ala Arg Ala Met Ser Ile Pro Thr Ser Pro Thr Arg Ile
 385 390 395 400
 Ser Phe His Ser Ile Lys Gln Thr Ala Ala Val
 405 410

(2) INFORMATION FOR SEQ ID NO:5

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

CCCGGATGCC TACAGAGAAT GCCTGGAGGA TGGGACCTGG GCCTCAAGGG

(2) INFORMATION FOR SEQ ID NO:6

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

GATCAACTAC TCACAGTGTG AGCCCATTTT GGATGACAAG CAGAGGAAGT A 51

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GAC GCG GCA CTG CTC CAC AGC CTG CTG GAG GCC AAC TGC AGC CTG	48
Met Asp Ala Ala Leu Leu His Ser Leu Leu Glu Ala Asn Cys Ser Leu	
1 5 10 15	
GCG CTG GCT GAA GAG CTG CTC TTG GAC GGC TGG GGG CCA CCC CTG GAC	96
Ala Leu Ala Glu Glu Leu Leu Leu Asp Gly Trp Gly Pro Pro Leu Asp	
20 25 30	
CCC GAG GGT CCC TAC TCC TAC TGC AAC ACG ACC TTG GAC CAG ATC GGA	144
Pro Glu Gly Pro Tyr Ser Tyr Cys Asn Thr Thr Leu Asp Gln Ile Gly	
35 40 45	
ACG TGC TGG CCC CGC AGC GCT GCC GGA GCC CTC GTG GAG AGG CCG TGC	192
Thr Cys Trp Pro Arg Ser Ala Ala Gly Ala Leu Val Glu Arg Pro Cys	
50 55 60	
CCC GAG TAC TTC AAC GGC GTC AAG TAC AAC ACG ACC CGG AAT GCC TAT	240
Pro Glu Tyr Phe Asn Gly Val Lys Tyr Asn Thr Thr Arg Asn Ala Tyr	
65 70 75 80	
CGA GAA TGC TTG GAG AAT GGG ACG TGG GCC TCA AAG ATC AAC TAC TCA	288
Arg Glu Cys Leu Glu Asn Gly Thr Trp Ala Ser Lys Ile Asn Tyr Ser	
85 90 95	
CAG TGT GAG CCC ATT TTG GAT GAC AAG CAG AGG AAG TAT GAC CTG CAC	336

Gln	Cys	Glu	Pro	Ile	Leu	Asp	Asp	Lys	Gln	Arg	Lys	Tyr	Asp	Leu	His	
			100					105					110			
TAC	CGC	ATC	GCC	CTT	GTC	GTC	AAC	TAC	CTG	GGC	CAC	TGC	GTA	TCT	GTG	384
Tyr	Arg	Ile	Ala	Leu	Val	Val	Asn	Tyr	Leu	Gly	His	Cys	Val	Ser	Val	
			115				120					125				
GCA	GCC	CTG	GTG	GCC	GCC	TTC	CTG	CTT	TTC	CTG	GCC	CTG	CGG	AGC	ATT	432
Ala	Ala	Leu	Val	Ala	Ala	Phe	Leu	Leu	Phe	Leu	Ala	Leu	Arg	Ser	Ile	
			130			135					140					
CGC	TGT	CTG	CGG	AAT	GTG	ATT	CAC	TGG	AAC	CTC	ATC	ACC	ACC	TTT	ATC	480
Arg	Cys	Leu	Arg	Asn	Val	Ile	His	Trp	Asn	Leu	Ile	Thr	Thr	Phe	Ile	
					150					155					160	
CTG	CGA	AAT	GTC	ATG	TGG	TTC	CTG	CTG	CAG	CTC	GTT	GAC	CAT	GAA	GTG	528
Leu	Arg	Asn	Val	Met	Trp	Phe	Leu	Leu	Gln	Leu	Val	Asp	His	Glu	Val	
				165					170					175		
CAC	GAG	AGC	AAT	GAG	GTC	TGG	TGC	CAC	TGC	ATC	ACC	ACC	ATC	TTC	AAC	576
His	Glu	Ser	Asn	Glu	Val	Trp	Cys	His	Cys	Ile	Thr	Thr	Ile	Phe	Asn	
			180					185					190			
TAC	TTC	GTG	GTG	ACC	AAC	TTC	TTC	TGG	ATG	TTT	GTG	GAA	GGC	TGC	TAC	624
Tyr	Phe	Val	Val	Thr	Asn	Phe	Phe	Trp	Met	Phe	Val	Glu	Gly	Cys	Tyr	
			195				200					205				
CTG	CAC	ACG	GCC	ATT	GTC	ATG	ACC	TAC	TCC	ACT	GAG	CGC	CTG	CGC	AAG	672
Leu	His	Thr	Ala	Ile	Val	Met	Thr	Tyr	Ser	Thr	Glu	Arg	Leu	Arg	Lys	
			210			215					220					
TGC	CTC	TTC	CTC	TTC	ATC	GGA	TGG	TGC	ATC	CCC	TTC	CCC	ATC	ATC	GTC	720
Cys	Leu	Phe	Leu	Phe	Ile	Gly	Trp	Cys	Ile	Pro	Phe	Pro	Ile	Ile	Val	
					230					235					240	
GCC	TGG	GCC	ATC	GGC	AAG	CTC	TAC	TAT	GAG	AAT	GAA	CAG	TGC	TGG	TTT	768
Ala	Trp	Ala	Ile	Gly	Lys	Leu	Tyr	Tyr	Glu	Asn	Glu	Gln	Cys	Trp	Phe	
				245					250				255			
GGC	AAG	GAG	CCT	GGC	GAC	CTG	GTG	GAC	TAC	ATC	TAC	CAA	GGC	CCC	ATC	816
Gly	Lys	Glu	Pro	Gly	Asp	Leu	Val	Asp	Tyr	Ile	Tyr	Gln	Gly	Pro	Ile	
			260					265					270			
ATT	CTC	GTG	CTC	CTG	ATC	AAT	TTC	GTA	TTT	CTG	TTC	AAC	ATC	GTC	AGG	864
Ile	Leu	Val	Leu	Leu	Ile	Asn	Phe	Val	Phe	Leu	Phe	Asn	Ile	Val	Arg	
			275				280					285				
ATC	CTA	ATG	ACA	AAG	TTA	CGC	GCG	TCC	ACC	ACA	TCC	GAG	ACA	ATC	CAG	912
Ile	Leu	Met	Thr	Lys	Leu	Arg	Ala	Ser	Thr	Thr	Ser	Glu	Thr	Ile	Gln	
			290			295					300					
TAC	AGG	AAG	GCA	GTG	AAG	GCC	ACC	CTG	GTG	CTC	CTG	CCC	CTC	CTG	GGC	960
Tyr	Arg	Lys	Ala	Val	Lys	Ala	Thr	Leu	Val	Leu	Leu	Pro	Leu	Leu	Gly	
					310				315						320	
ATC	ACC	TAC	ATG	CTC	TTC	TTC	GTC	AAT	CCC	GGG	GAG	GAC	GAC	CTG	TCA	1008
Ile	Thr	Tyr	Met	Leu	Phe	Phe	Val	Asn	Pro	Gly	Glu	Asp	Asp	Leu	Ser	

	325	330	335	
CAG ATC ATG TTC ATC TAT TTC AAC TCC TTC CTG CAG TCG TTC CAG GGT				1056
Gln Ile Met Phe Ile Tyr Phe Asn Ser Phe Leu Gln Ser Phe Gln Gly				
	340	345	350	
TTC TTC GTG TCT GTC TTC TAC TGC TTC TTC AAT GGA GAG GTG CGC TCA				1104
Phe Phe Val Ser Val Phe Tyr Cys Phe Phe Asn Gly Glu Val Arg Ser				
	355	360	365	
GCC GTG AGG AAG AGG TGG CAC CGC TGG CAG GAC CAT CAC TCC CTT CGA				1152
Ala Val Arg Lys Arg Trp His Arg Trp Gln Asp His His Ser Leu Arg				
	370	375	380	
GTC CCC ATG GCC CGG GCC ATG TCC ATC CCT ACA TCA CCC ACA CGG ATC				1200
Val Pro Met Ala Arg Ala Met Ser Ile Pro Thr Ser Pro Thr Arg Ile				
	385	390	395	400
AGC TTC CAC AGC ATC AAG CAG ACG GCC GCT GTG TGACCCCTCG GTCGCCACCC				1253
Ser Phe His Ser Ile Lys Gln Thr Ala Ala Val				
	405	410		
TGCACAGCTC CCCTGTCCTC CTCCACCTTC TTCCTCTGGG TTCTCTGTGC TGGGCAGGCT				1313
CTCGTGGGGC AGGAGATGGG AGGGGAGAGA CCAGCTCTCC AGCCTGGCAG GAAAGAGGGG				1373
GTGCGGCAGC CAAGGGGGAC TGCAAGGGAC AGGGATGAGT GGGGGCCACC AGGCTCAGCG				1433
CAAGAGGAAG CAGAGGGAAT TCGATGGTGG AGCTC				1468

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asp Ala Ala Leu Leu His Ser Leu Leu Glu Ala Asn Cys Ser Leu
1 5 10 15

Ala Leu Ala Glu Glu Leu Leu Leu Asp Gly Trp Gly Pro Pro Leu Asp
20 25 30

Pro Glu Gly Pro Tyr Ser Tyr Cys Asn Thr Thr Leu Asp Gln Ile Gly
35 40 45

Thr Cys Trp Pro Arg Ser Ala Ala Gly Ala Leu Val Glu Arg Pro Cys
50 55 60

Pro Glu Tyr Phe Asn Gly Val Lys Tyr Asn Thr Thr Arg Asn Ala Tyr
65 70 75 80

Arg Glu Cys Leu Glu Asn Gly Thr Trp Ala Ser Lys Ile Asn Tyr Ser
 85 90 95
 Gln Cys Glu Pro Ile Leu Asp Asp Lys Gln Arg Lys Tyr Asp Leu His
 100 105 110
 Tyr Arg Ile Ala Leu Val Val Asn Tyr Leu Gly His Cys Val Ser Val
 115 120 125
 Ala Ala Leu Val Ala Ala Phe Leu Leu Phe Leu Ala Leu Arg Ser Ile
 130 135 140
 Arg Cys Leu Arg Asn Val Ile His Trp Asn Leu Ile Thr Thr Phe Ile
 145 150 155 160
 Leu Arg Asn Val Met Trp Phe Leu Leu Gln Leu Val Asp His Glu Val
 165 170 175
 His Glu Ser Asn Glu Val Trp Cys His Cys Ile Thr Thr Ile Phe Asn
 180 185 190
 Tyr Phe Val Val Thr Asn Phe Phe Trp Met Phe Val Glu Gly Cys Tyr
 195 200 205
 Leu His Thr Ala Ile Val Met Thr Tyr Ser Thr Glu Arg Leu Arg Lys
 210 215 220
 Cys Leu Phe Leu Phe Ile Gly Trp Cys Ile Pro Phe Pro Ile Ile Val
 225 230 235 240
 Ala Trp Ala Ile Gly Lys Leu Tyr Tyr Glu Asn Glu Gln Cys Trp Phe
 245 250 255
 Gly Lys Glu Pro Gly Asp Leu Val Asp Tyr Ile Tyr Gln Gly Pro Ile
 260 265 270
 Ile Leu Val Leu Leu Ile Asn Phe Val Phe Leu Phe Asn Ile Val Arg
 275 280 285
 Ile Leu Met Thr Lys Leu Arg Ala Ser Thr Thr Ser Glu Thr Ile Gln
 290 295 300
 Tyr Arg Lys Ala Val Lys Ala Thr Leu Val Leu Leu Pro Leu Leu Gly
 305 310 315 320
 Ile Thr Tyr Met Leu Phe Phe Val Asn Pro Gly Glu Asp Asp Leu Ser
 325 330 335
 Gln Ile Met Phe Ile Tyr Phe Asn Ser Phe Leu Gln Ser Phe Gln Gly
 340 345 350
 Phe Phe Val Ser Val Phe Tyr Cys Phe Phe Asn Gly Glu Val Arg Ser
 355 360 365
 Ala Val Arg Lys Arg Trp His Arg Trp Gln Asp His His Ser Leu Arg
 370 375 380

Val Pro Met Ala Arg Ala Met Ser Ile Pro Thr Ser Pro Thr Arg Ile
385 390 395 400

Ser Phe His Ser Ile Lys Gln Thr Ala Ala Val
405 410